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US-08-469-318-77
US-08-468-609A-68
US-08-468-609A-70
US-08-468-609A-71
US-08-468-609A-73
US-08-468-609A-77
US-08-468-609A-77
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US-08-6-609A-77
US-08-6-609A-77
US-08-6-609A-67
US-08-6-609A-67
US-08-6-609A-67
US-08-469-318-67
US-08-469-318-67
US-08-469-318-67
                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: YOSHIDA, HAJIME
APPLICANT: YOSHINORI, KOMATSU
TITLE OF INVENTION: NOVEL POLYPEPTIDES
NUMBER OF SEQUENCES: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 306799/86
FILING DATE: 23-DEC-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 51357/88
FILING DATE: 04-MAR-1988
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 80088/88
FILING DATE: 31-MAR-1988
ATTORNEY/AGENT INFORMATION:
NAME: CRAWFORD, ARTHUR
REGISTRATION NUMBER: 25327
REFERENCE/DOCKET NUMBER: 249-73
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,411
FILING DATE: 03-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: NIXON & VANDERHYE P. 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08434111
Patent No. 5681720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KUGA, TETSURO
MIYAJI, HIROMASA
SATO, MORIYUKI
OKABE, MASAMI
MORIMOTO, MAKOTO
ITOH, SEIGA
YAMASAKI, MOTO
YOKOO, YOSHIHARU
YAMAGUCHI, KAZUO
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(703)816-4100
   CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & V
STREET: 1100 NORTH G
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Patent No. 5194592
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Sequence 178
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Sequence 178
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
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                 version 4.5
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PCT-US95-01185-78
PCT-US95-01185-84
US-08-469-318-68
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US-08-890-640-1
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Version #1.30

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                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: US/08/434,402 FILING DATE: 03-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.3%; Score 486.8; DB 1;
98.6%; Pred. No. 2.3e-109;
ive 0; Mismatches 7;
                                                                                                                                                                                                                                                                               FILING DATE: 03-MAY-1995
CLASSIFTCATION: 530
PRIOR APPLICATION DATE: 30
PRIOR APPLICATION DATE: 30-DEC-1986
FILING DATE: 23-DEC-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 51357/88
FILING DATE: 04-MAR-1988
PRIOR APPLICATION NUMBER: JP 80088/88
FILING DATE: 31-MAR-1988
ATTORNEY AGENT INFORMATION:
                                                   3: NIXON & VANDERHYE P.C. 1100 NORTH GLEBE ROAD
                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: CRAWFORD, ARTHUR
REGISTRATION NUMBER: 25327
REFERENCE/DOCKET NUMBER: 249-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703)816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 525 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 98.6
Matches 491; Conservative
                    NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                        ZIP: 22201-4714
COMPUTER READABLE FORM:
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CTHER INFORMATION:
CTHER INFORMATION:
US-08-434-402-1
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                                                                                                           VIRGINIA
                                                                                                                             COUNTRY: U.S.A.
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                                                      ADDRESSEE:
STREET: 11
                                                                                                       STATE:
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                                                                                                                                                                                                                                                                                     Length 525;
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                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                   Score 486.8; DB 1;
Pred. No. 2.3e-109;
0; Mismatches 7;
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US-08-434-402-1
Sequence 1, Application US/08434402
; Patent No. 5714581
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MIYAJI, HIROMASA
SATO, MORIVUKI
OKABE, MASAMI
MORIMOTO, MAKOTO
ITOH, SEIGA
YAMASAKI, MOTOO
YOKOO, YOSHIHARU
YAMAGUCHI, KAZUO
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                                                                                                                                                                                                                                                                                 93.3%;
ilarity 98.6%;
Conservative 0
                                                                                                                        MOLECULE TYPE: DNA (genomic)
TELEX: 200797 NIXN UR INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 525 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        505 CGCCACCTTGCCCAGCCC 522
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                                                                                                                                                            NAME/KEY: CDS
LOCATION: 1..522
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                           linear
                                                                                                                                                                                                                                                                                                   Similarity
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Length 525;

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                                                                                                                                                                                                                                     Score 486.8; DB 1;
Pred. No. 2.3e-109;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: YOSHINORI, KOMATSU
TITLE OF INVENTION: NOVEL POLYPEPTIDES
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08890640 Patent No. 5994518
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MIYAJI, HIROMASA
SATO, MORIYUKI
OKABE, MASAMI
MORIMOTO, MAKOTO
ITOH, SEIGA
YAMASAKI, MOTOO
YOKOO, YOSHHARU
                                                                           DNA (genomic)
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98.6%;
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LENGTH: 525 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                         Query Match 93.3
Best Local Similarity 98.6
Matches 491; Conservative
                                                                                                                           LOCATION: 1.522
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                              NAME/KEY: CDS
                                                        TOPOLOGY: 1i
MOLECULE TYPE:
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US-08-890-640-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: YAMASAKI, MOTOO
APPLICANT: YOKOO, YOSHIHARU
APPLICANT: YAMAGUCHI, KAZUO
APPLICANT: YOSHIDA, HAJIME
APPLICANT: YOSHINORI, KOMATSU
TITLE OF INVENTION: NOVEL POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/434,411
FILING DATE: 03-MAY-1995
APPLICATION NUMBER: JP 306799/86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARPLICATION NUMBER: JP 306799/86 FILING DATE: 23-DEC-1986 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 51357/88 FILING DATE: 04-MAR-1988 APPLICATION APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/783,288
FILING DATE: 10-JAN-1997
CLASSIFICATION: 536
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 25327
REFERENCE/DOCKET NUMBER: 249
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                    KUGA, TETSURO
MIYAJI, HIROMASA
SATO, MORIYUKI
OKABE, MASAMI
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ITOH, SEIGA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CLASSIFICATION:
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APPLICANT:
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385 GCCCTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCTTTCCAGCGCGGGCA
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                                                                     385 GCCCTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCTCTGCTTTCCAGCGCCGGGCA
                  RESULT 5
5194592-25
; Patent No. 5194592
APPLICANT: YOSHIDA, HAJIME
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO NOVEL
; POLYPEPTIDES DERIVITIVES OF HUMAN GRANULOCYTE COLONY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.3%; Score 486.8; DB 6;
98.6%; Pred. No. 2.3e-109;
11ve 0; Mismatches 7;
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APPLICATION NUMBER: US/07/318,527
FILING DATE: 3-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 136,647
FILING DATE: 22-DEC-1987
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Matches 491; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               STIMULATING FACTOR
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; LENGTH: 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "HUMAN GRANULOCYTE COLONY STIMULATING FACTOR"
                                                                                                                                    SOFTWARE: PACTONS/MS-DOS SOFTWARE: PACTONS/MS-DOS SOFTWARE: PACTONIN Release #1.0, Version #1.30 CURRET APPLICATION DATA:
APPLICATION NUMBER: US/08/890,640
                                                                                                                                                                                                                                         PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/434,411
FILING DATE: 32 DEC.1995
APPLICATION NUMBER: JP 306799/86
FILING DATE: 23 DEC.1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 51357/88
FILING DATE: 04-MAR.1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8008/88
FILING DATE: 31-MAR.1988
ATORNEY/AGENT INFORMATION:
NAME: CRANFORD, ARTHUR
REGISTRATION NUMBER: 25327
REFERENCE/DOCKET NUMBER: 249-73
TELECOMMUNICATION INFORMATION:
NAME: CRANFORD.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
VANDERHYE P.C.
                                                                                  ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-
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TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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Matches 491; Conservative
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                               ARLINGTON
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                                                                     COUNTRY: U.S.A.
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                           Gaps
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Length 525;
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62 TGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAGC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  546;
                                                                                                                                                      Multivariant IL-3 Hematopoiesis Fusion
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                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT AFFICATION DATA:
APPLICATION NUMBER: US/08/469,318
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   488 IGGAGGIGICGIACCGCGIICIACGCCACCIIGCGCAGCCC 528
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Pred. No. 2.1e-106;
0; Mismatches 29;
                                                                                 Sequence 178, Application US/08469318
Patent No. 6022535
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Multivariant I
                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/446,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: DNA (genomic) US-08-469-318-178
                                                                                                                                                                      Protein
196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 90.9%;
Best Local Similarity 94.4%;
Matches 492; Conservative
                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                   RESULT 7
US-08-469-318-178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCACCTTGGACACACTGCAGCTGGACGTCGCCGACTTTGCCACCACCATCTGGCAGCAGA 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 546;
                                                                                                                                                      Multivariant IL-3 Hematopoiesis Fusion
Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                 TITLE OF INVENTION: Multivariant IL-3 Hematopoies TITLE OF INVENTION: Protein NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCCAGCCC 522
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                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/469,318
                                                                                                 Sequence 177, Application US/08469318
Patent No. 6022535
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
INFORMATION FOR SEQ ID NO: 17
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
505 cgccaccttgcccagccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              double
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nes 492; Conserv
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                                                                                                                                                                                                                                                                                                                                         FILING DATE
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                                                                                   US-08-469-318-177
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Best Local S
Matches 492,
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APPLICANT: Braford-Goldberg, Sarah R.
APPLICANT: Braford-Goldberg, Sarah R.
APPLICANT: Caparon, Maire H.
APPLICANT: Easton, Alan M.
APPLICANT: McKearn, John P.
APPLICANT: McKearn, John P.
APPLICANT: Thomas, John W.
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (I WUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                        427
188 TGAGCTCCTGCCCCAGGCCCTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATAGCG 247
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                                                                                                                                                                                                                                              422 CCTCTGCTTTCCAGGGGCGGGCAGGAGGGTCCTAGTTGCCTCCCATCTGCAGAGCTTCC 481
                                                                                        248 GCCTTTTCCTCTACCAGGGCTCCTGCAGGCCCTGGAAGGGATATCCCCCGGAGTTGGGTC
                                                                                                                                                                                                                                                                      482 TGGAGGTGTCGTACCGCGTTCTACGCCCACCTTGCCCAGCCC 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: US/08/468,609A FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bauer, S. C.
Braford-Goldberg, Sarah R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 178, Application US/08468609A; Patent No. 6030812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60680
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (314)737-6986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (314)/3/ UNCORNATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS: LENGTH: 546 base pairs TYPE: nucleic acid TYPE: TYPE: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
APPLICANT: Bauer, S. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Chicago
STATE: Illinois
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CLASSIFICATION:
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US-08-468-609A-178
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APPLICANT: Bracord-Goldberg, Sarah R.
APPLICANT: Bracord-Goldberg, Sarah R.
APPLICANT: Caparon, Maire H.
APPLICANT: Easton, Alare H.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Paik, Kumnan
APPLICANT: Thomas, John W.
APPLICANT: Thomas, John W.
APPLICANT: Poins Paik, Kumnan
APPLICANT: Poins Paik, Kumnan
APPLICANT: Thomas, John W.
APPLICANT: Poins SEQUENCES: 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co., ADDRESSEE: Corporate Patent Dept.
STREET: P. O. Box 5110
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CURRENT APPLICATION DATA:
ELICATION NUMBER: US/08/468,609A
FILING DATE: 06-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Bennett, Dennis A.
RECISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                    Sequence 177, Application US/08468609A Patent No. 6030812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 177: SEQUENCE CHARACTERISTICS: LENGTH: 546 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                     Abrams, Mark A.
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: P. O. BOX CITY: Chicago STATE: Illinois COUNTRY: USA
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                                                                                                                              GENERAL INFORMATION:
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                                                               US-08-468-609A-177
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US-08-468-609A-177
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Best Local Simi
Matches 492;
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SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                    Matches 492; Conservative
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                                      Query Match
Best Local Similarity
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MOLECULE TYPE:
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                                                                  Length 546;
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APPLICATION NUMBER: PCT/MGGE **
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                                                                 Score 474.6; DB 3;
Pred. No. 2.1e-106;
0; Mismatches 29;
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APPLICATION NUMBER: US 08/192325
FILLING DATE: 14-FBE-1994
INFORMATION FOR SEQ ID NO: 177:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
TITLE OF INVENTION: Multivarian'
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIAN
OPERATING SYSTEM: PC-DOS/MS-DC
SOFTWARE: PatentIn Release #1.
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-468-609A-178
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MOLECULE TYPE: DNA (genomic)
                                                                 Query Match 90.9%;
Best Local Similarity 94.4%;
Matches 492; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
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                                        Gaps
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  546;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  Length
                                        Indels
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APPLICATION NUMBER: PCT/US95/01185
FILING DATE: 02-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     488 TGGAGGTGTGTACCGCGTTCTACGCCACCTTGCGCAGCCC 528
Score 474.6; DB 5;
Pred. No. 2.1e-106;
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                                        0; Mismatches
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APPLICANT:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192325
FILING DATE: 14-FEB-1994
INFORMATION FOR SEQ ID NO: 178:
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                             Gaps
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  Length 546;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                             Indels
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  ; DB 5;
.1e-106;
             Pred. No. 2.16
0; Mismatches
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APPLICATION NUMBER: US/08/469,318
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,872
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90.9%;
ilarity 94.4%;
Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 921 base pairs
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STRANDEDNESS: double
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               Similarity
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                          Matches 492;
  Query Match
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                                      Gaps
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Length 921;
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TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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PatentIn Release #1.0, Version #1.30 (EPO)
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Pred. No. 2.3e-106;
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                                  0; Mismatches
90.9%; Score 474.6; 94.4%; Pred. No. 2.30
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Patent No. 6022535
GENERAL INFORMATION:
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APPLICATION NUMBER: 08/446,872
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SEQUENCE CHARACTERISTICS:
LENGTH: 921 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                     Best Local Similarity 94.4
Matches 492; Conservative
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APPLICATION NUMBER: US
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                   Similarity
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US-08-469-318-75
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US-08-469-318-75
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Query Match
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    Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
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Pred. No. 2.3e-106;
); Mismatches 29;
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    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 84, Application US/08469318
Patent No. 6022535
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Multivariant
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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; MOLECULE TYPE: DNA (genomic)
US-08-469-318-84
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TYPE: nucleic acid
STRANDEDNESS: double
    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA APPLICATION NUMBER: US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
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                 Gaps
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                Indels
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 Pred. No. 2.3e-106;
); Mismatches 29;
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Pred. No. 2.3e-106;
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TITLE OF INVENTION: Multivariant III-
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,318
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,872
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; Patent No. 6022535
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 94.48;
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94.4%;
             Matches 492; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
Best Local Similarity
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Best Local Similarity
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US-08-469-318-78
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2 CGCCAACATATCGCGCCTCGAGTCTACCACAGAGCTTCCTTTTAAAAAGCTTAGAGCAAG
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1736436 seqs, 858457221 residues
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Location/Qualifiers

Homo sapiens

sig_peptide mat_peptide

1..63 /*tag= a 64..1047 /*tag= b

Description	Fusion peptide #1	Fusion peptide #3	Fusion peptide #2	Plasmid pASN6 enco	Plasmid pASN145 en	Plasmid pAS28 enco	G-CSF gene isolate	Human hG-CSF gene	Human hG-CSF gene
SUMMARIES	AAT41786	AAT41788	AAT41787	AAQ04482	AAQ04484	AAQ04481	AAN80947		
DB	17	17	17	11	11	11	6	22	22
Length	1047	1095	1083	525	525	525	525	531	615
% Query Match	100.0	100.0	99.7	98.5	97.9	6.96	93.3	93.3	93.3
% Query Score Match Length DB I	522	522	520.4	514	510.8	206	486.8	486.8	486.8
Result No.	1	7	m	4	Ŋ	9	7	œ	6

(KYOW) KYOWA HAKKO KOGYO KK

96WO-JP01157. 95JP-0102625.

26-APR-1996;

26-APR-1995;

WO9634016-A1

31-OCT-1996.

	pWON13026 DPMON13026 DPMON13026 DPMON130151 DPMON13151 DPMON13151 DPMON1306 DPMON1308 DPMON	I TPO activity. colony stimulating factor; hG-CSF;
AAN70223 AAN71320 AAN60937 AAN81478 AAN91086 AAN71089 AAN771848 AAQ97205 AAA03773 AAA03772	AAQ97186 AAQ97189 AAQ97189 AAQ97189 AAA03746 AAA03746 AAA03752 AAA037187 AAQ97187 AAQ97187 AAQ97187 AAQ97187 AAQ97187 AAA03738 AAA03738 AAA03741 AAA03741 AAA03741 AAA03741 AAA03741 AAA03741 AAA03741 AAA03741 AAA03741 AAA03741	BP. SF and Ti cocyte co. peptide;
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10 11 12 13 14 15 17 17 19	11000000000000000000000000000000000000	RESULT AAT41786 ID AAT XX XX XX XX AC AC XX

#3 having G-CSF and TPO activity.

Fusion peptide

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                                                                             activity -
glycol, used for
                                                                                                                                                  The sequences given in AAT41786-88 encode fusion proteins which are composed of a peptide having human granulocyte colony stimulating factor (hG-CSF) activity fused with a peptide having thrombopoletin (TPO) activity, opt. via a spacer peptide. Peptides derived from these by deletion, insertion or substitution of one or more amino acid residues are included within the scope of the invention. The fusion peptides stimulate blood platelet and leukocyte production and are useful in the treatment of anaemia.
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                                                                                                                                                                                                                                                                                                              Length 1047;
 Terasaki
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                                                                         Fusion peptide having G-CSF and with thrombopoietin optionally chemically modified with a poly:alkylene
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100.0%; Pred. No. 2.7e-109;
ive 0; Mismatches 0;
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 Tamaoki T,
Yokoi H;
 Shiotsu Y,
Yamashita K,
                                                                                                                           Claim 3; Page 46-48; 71pp; Japanese.
                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 100.
Matches 522; Conservative
Konishi N,
             Uchida K, Yamasaki M,
                                                                                      optionally chemically treatment of anaemia
                                     WPI; 1996-497573/49
                                               P-PSDB; AAW00377
 Anazawa H,
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                  Fusion protein; human granulocyte colony stimulating factor; hG-CSF; thrombopoietin; TPO; spacer peptide; blood platelet production; leukocyte production; anaemia; ds.
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llarity 100.0%; Pred. No. 2.7e-109;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequences given in AAT41786-88 encode fusion
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Yokoi H;
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                                                                                                                                                                                                                                                                                                             Shiotsu Y,
Yamashita K,
                                                                                                    Location/Qualifiers
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                                                                          Homo sapiens
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Matches 522
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Pred. No.
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 Best Local Similarity 99.8 Matches 521; Conservative
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GCCTCTGCTTTCCAGCGCCGGGCAGGGGGTCCTAGTTGCCTCCCATCTGCAGAGCTTC
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Yamashita K,
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P-PSDB; AAW00378.
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99.7%; Score 520.4; DB 17; Length 1083;

Query Match

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0; Mismatches
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GIGAGGAAGAICCAGGGCGAIGGCGCAGCGCTCCAGGAGGAAGCIGIGIGCCACCIACAAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptide(s) with added carbohydrate chains - forme modification of amino acid sequence, used to improve physiochemical properties and/or activities.
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Pred. No. 8.6e-107;
); Mismatches 7; 1
                                                                                                                                                                                                                                                                                                                                                     /label-synthetic_mutation
/note-"old seq (ctgggccctgcc)"
misc_difference 49..51
                                                                                                Granulocyte stimulating factor; glycosylation;
                                                                                                                                                                                                                                          /label-synthetic_mutation
/note="old seq (acc)"
misc_difference 7..18
                                                Plasmid pASN145 encoding hG-CSF[ND28N145].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label=synthetic_mutation
/note="old seq (cag)"
misc_difference 439..441
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/note-"old seq (cgg)"
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/note="old seq (tgc)"
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Best Local Similarity 98.7%;
Matches 515; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89EP-0117981
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04-OCT-1990 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasaki K, Nishi T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1990-165029/22
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                                                                                                                                                                                                                     misc_difference
                                                                                                                                                   Homo sapiens
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Pred. No. 1.6e-107;
0; Mismatches 5;
                                                                                                                                                                                                                                          Polypeptide(s) with added carbohydrate chains modification of amino acid sequence, used to physiochemical properties and/or activities.
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99.0%;
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Best Local Similarity 99.0
Matches 517; Conservative
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                                                                                                                     Sasaki K, Nishi T,
                                                                                                                                                                     WPI; 1990-165029/22.
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                         CTGAGCAGCTGCCCCAGCCAGGCCCTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATAGC
                                                                             CCCACCTTGGACACACTGCAGCTGGACGTCGCCGACTTTGCCACCACCATCTGGCAGCAG
                                                                                                                    atggaagaactgggaatggccctgcctgcagcccacccagggtgccatgccggccttc
                                                                                                       GCCTCTGCTTTCCAGCGCCGGGCAGGGGGTCCTAGTTGCCTCCCATCTGCAGAGCTTC
                                                                                                              Polypeptide(s) with added carbohydrate chains - formed by
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/note="old seq (ctgggcct)
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P-PSDB; AAR05113.
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                                                                                                         The sequence encodes a deriv. of mature hG-CSF, designated hG-CSF[N28] which has 5 amino acid substns. This results in one axtra 0-1inked glycoslation site giving the new protein improved stability and activity.
                                                                                                                                                                                                                                                                                                                         Length 525;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G-CSF gene isolated from peripheral blood macrophages
modification of amino acid sequence, used to improve physiochemical properties and/or activities.
                                                                                                                                                                                                                                                   T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 CTGGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCCAGCCC 522
                                                                                                                                                                                                                                                                                                                         96.9%; Score 506; DB 11; 98.1%; Pred. No. 1.1e-105;
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                                                                                                                                                                                                                                                   Sequence 525 BP; 94 A; 184 C; 149 G; 98
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                                                                                                                                                                                                                                                                                                                                                                                                 25 CTACCACAGAGCTTCCTTTTAAAAGCTTAGAGCAAGTGAGGAAGATCCAGGGCGATGGC 84
                                                                                                                                                                                                                                                                                                                                                                                                              The sequence is carried on plasmid pCSF1-2 isolated from a CDNA places. In the pepared from mRNA extracted from peripheral blood macrophages. It encodes a protein whose As sequence agrees with those determined for G-CSF from the human squamous cell line CHU-II and the human bladder cancer cell line 5637. It can be used as a "master gene" for the construction of mutant genes which encode variants of hG-CSF which differ by at least one AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGCAGGCCCTGGAAGGGATCTCCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTG
                                                                                                                                                  polypeptide derivs. - giving high specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGCAGCTGCCAGGCTGCTTGAGCCAACTCCATAGCGGCCTTTTCCTCTACCAGGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctgcaggccctggaagggatctccccgagttgggtcccaccttggacacactgcagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACGTCGCCGACTTTGCCACCACCATCTGGCAGCAGATGGAAGTGGGAATGGCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCCTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCTCTGCTTTCCAGCGCCGGGCA
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O
                                                                                                                                                                                                                                                                                                                                                       Length 525;
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                    Sequence 525 BP; 85 A; 192 C; 151 G; 97 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                       DB 9;
                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 2.4e-101;
0; Mismatches 7;
                                                                                                                                                Human granulocyte colony stimulating factor having at least one different amino acid, activity and stability.
                                                                                                                                                                                                                                                                                                                                                       Score 486.8;
                                                                                ×
                                                                                 Sato
                                                                                         Yamaguchi K;
                                                                                                                                                                                                                                                                                              See also AAN80945 and AAN80946.
                                                                               Komatsu Y, Miyaji H,
                                                                                                                                                                                                                                                                                                                                                     93.3%;
                                                         (KYOW ) KYOWA HAKKO KOGYO KK.
             87EP-0119157.
                                   86JP-0306799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         522
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                                                                                                                                                                                             Disclosure; ; pp; English.
                                                                                                                                                                                                                                                                                                                                                                             Matches 491; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yokoo Y,
                                                                                                               WPI; 1988-176825/26.
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                           P-PSDB; AAP80965
             23-DEC-1987;
                                   23-DEC-1986;
                                                                                           Yamasakı M,
                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                               Kuqa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205
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the invention relates to an Escherichia coll producing and secreting human granulocyte colony stimulating factor (hG-CSF), more specifically, to a recombinant plasmid constructed to express secretory hG-CSF in E. coli, an E. coli transformed with that plasmid to secrete hG-CSF, and a process for preparing hG-CSF using the transformed hG-CSF. The recombinant plasmid vector comprises of a kanamycin resistance gene, a promoter, an endoxylanase signal sequence, a nucleotide sequence coding for an oligopeptide consisting of 13 amino acids including consecutive histidine residues and a hG-CSF. E.coli transformed with recombinant plasmid vector is useful for preparing hG-CSF. The method comprises culturing the microorganism to obtain a hG-CSF fusion protein and treating the fusion protein with a protease preferably Factor Xa, to obtain a hG-CSF, where the fusion protein is obtained from the culture by employing Ni-column. The present sequence is human hG-CSF gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant plasmid vector comprising an endoxylanase signal sequence, human granulocyte colony stimulating factor gene and other components, when transformed into microorganism useful for preparing the colony
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                                                                                                                                                                                                                              granulocyte colony stimulating factor; hG-CSF; protease; Xa; kanamycin resistance; endoxylanase signal peptide; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Human hG-CSF protein'
                                                                                                                                                                     Human hG-CSF gene inserted into plasmid pEDCSFm
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Pred. No. 2.4e-101;
0; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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Best Local Similarity 98.6%;
Matches 491; Conservative
AAD19772 standard; DNA; 531
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/product=
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                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                               18-DEC-2001
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                                                      AAD19772;
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                                                                                                                                                                                                                                 Human;
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human granulocyte colony stimulating factor (hG-CSF), more specifically, to a recombinant plasmid constructed to express secretory hG-CSF in E. coli, an E. coli transformed with that plasmid to secrete hG-CSF and a process for preparing hG-CSF using the transformed hG-CSF. The recombinant plasmid vector comprises of a kanamycin resistance gene, a promoter, an endoxylanase signal sequence, a nucleotide sequence coding for an oligopeptide consisting of 13 amino acids including 6 consecutive histidine residues and a hG-CSF. E. coli transformed with recombinant plasmid vector is useful for preparing hG-CSF. The method comprises bulturing the microorganism to obtain a hG-CSF fusion protein and treating the fusion protein is obtained from the culture obtain a hG-CSF, where the fusion protein is obtained from the culture by employing Ni-column. The present sequence is human hG-CSF gene
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                                                                                                                                                                                                                                     The invention relates to an Escherichia coli producing and secreting
                                                                                            208 ctgcagctggcaggctgcttgagccaactccatagcggccttttcctctaccagggggttc
                                                                                                                              GACGTCGCCGACTTTGCCACCACCATCTGGCAGATGGAAGAACTGGGAATGGCCCCT
                                                                                                                                                                            GCCCTGCAGCCCAGGGTGCCATGCCGGCCTTCGCCTCTGCTTTCCAGCGCCGGGCA
                                                                                                                                                                                                                        GGAGGGGTCCTAGTTGCCTCCCATCTGCAGAGCTTCCTGGAGGTGTCGTACCGCGTTCTA
                                                                                CTGCAGGCCCTGGAAGGGATCTCCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                              granulocyte colony stimulating factor; hG-CSF; protease; Xa; kanamycin resistance; endoxylanase signal peptide; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "Human hG-CSF protein"
/note= "CDS does not include start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                         Human hG-CSF gene inserted into plasmid p19CSFm
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P-PSDB; AAE12153.
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                                                                                                                                                                                                                                                                                         CTGCTCGGACACTCTCTGGGCATCCCCTGGGCTCCCTGAGCAGCTGCCCCAGGCCAGGCC
                                                                                                                                                                                                                                                                                                         GACGTCGCCGACTTTGCCACCACCATCTGGCAGCAGATGGAAGTGGGAATGGCCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human granulocyte colony stimulating factor; G-CSF; leukaemia; ss
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0
                                                                                 Length 615;
                                                                                                                    Indels
                                 Sequence 615 BP; 105 A; 219 C; 178 G; 113 T; 0 other;
                                                                                 Score 486.8; DB 22;
Pred. No. 2.4e-101;
                                                                                                                    0; Mismatches
inserted into plasmid p19CSFm.
                                                                                 93.38;
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                                                                                                                  Matches 491; Conservative
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505 CGCCACCTTGCCCAGCCC
                                                   AAN71320 standard;
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                                                                                                                                     Homo sapiens
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04-OCT-1985;
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                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                        The plasmid
                                                                                                                                                                                                       The plasmid was isolated from a cDNA library prepd. from CHU-2 cells, a human oral cavity tumour cell line, using a 1500 bp insert from pBBG4 (AAN7022) and probe LC (AAN71351). The plasmid was used to prepare recombinant expression plasmids for the produ.
                                                                                                                                                                                                                                                                                                                        CTACCACAGAGCTTCCTTTTAAAAAGCTTAGAGCAAGTGAGGAAGATCCAGGGCGATGGC
                                                                                                                                                                                                                                                                                                                                              GCAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAGCTGTGCCACCCCGAGGAGCTGGTG
                                                                                                                                                                                                                                                                                                                                                     CTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATAGCGGCCTTTTTCCTCTACCAGGGGCTC
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                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                   Length 1520;
                                                                                                                                                          Polypeptide with human granulocyte colony stimulating factor activity - is obtd. by cultivating transformant formed by
                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                             other;
                                                                                                                                                                                                                                                                                 Score 486.8; DB 8;
Pred. No. 2.7e-101;
0; Mismatches 7;
                                                                                                                                                                                                                                                           Sequence 1520 BP; 303 A; 487 C; 402 G; 328 T; 0
                                                                                                                                                                                                                                              See also AAN70221-N70224 and AAN71349-N71351
Location/Qualifiers
31..645
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                                                                                                                                                                                         Disclosure; Fig 4; 73pp; English.
                                                                                                                      Tsuchiya
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                                                                                                                                                                                                                                                                                  93.3%;
98.6%;
                                                          86EP-0113446
                                                                         85JP-0217150
                                                                               86JP-0166710
86JP-0166709
                                                                                                                                                                        recombinant DNA procedures.
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                                                                                                      (CHUS ) CHUGAI SEIYAKU KK
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               /*tag=
                                                                                                                     Nagata S,
                                                                                                                                   WPI; 1987-124182/18.
P-PSDB; AAP70162.
                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                        30-SEP-1985;
17-JUL-1986;
17-JUL-1986;
                                                          30-SEP-1986;
                                           06-MAY-1987
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Matches 491;
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                             EP220520-A
                                                                                                                     Yamzaki T,
                                                                                                                                                                                                                                                                                   Query Match
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Sequence encoding human granulocyte colony stimulating factor (hGCSF)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                    therapy; neutropenia; eosinopenia; lymphopenia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1520 BP; 305 A; 488 C; 401 G; 326 T; 0
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neutrophiles - contains human granu
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85JP-0220450
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625 cgccaccttgcccagcc
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infection by anaerobic and aerobic bacteria and fungl.
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                                                                                                              GGAGGGGTCCTAGTTGCCTCCCATCTGCAGAGCTTCCTGGAGGTGTCGTACCGCGTTCTA 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The plasmid encodes a novel polypeptide having human graulocyte colony stimulating factor activity. The CSF may be produced either from a cell-line secreting the factor into its medium, or from a transformant microorganism. The product induces high immunity to
                                 CTGCAGGCCCTGGAAGGGATCTCCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTG
                                                       GACGTCGCCGACTTTGCCACCACCATCTGGCAGCAGAAGAAGAACTGGGAATGGCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Infection-protection inducing agent - contains human granulocyte colony stimulating factor obtd. by cell culture or recombinant
                                                                                                                                                                                                                                                    G-CSF; granulocyte colony stimulating factor; antimicrobial
                                                                                                                                                                                                                                      Plasmid pBRV2 insert encoding granulocyte CSF.
                                                                                                                                                                                                                                                                                                                                                                                                                      Matsumoto M;
                                                                                                                                                                                                                                                                               Location/Qualifiers
31..645
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121
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                                                                                                                                                                                          AAN60937 standard; DNA; 1521
                                                                                                                                          CGCCACCTTGCCCAGCCC 522
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                                                                                                                                                                                                                                                                                                                                                                                                (CHUS ) CHUGAI
(ONOM/) ONO M.
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03-DEC-1985;
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WO8604605-A.
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technology.
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                                                                                                                                                                                                                                                                                                         GCAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAGCTGTGCCACCCCGAGGAGCTGGTG
                                                                                                                                                                                   25 CTACCACAGAGCTTCCTTTTAAAAAGCTTAGAGCAAGTGAGGAAGATCCAGGGCGATGGC
                                                                                                                                       ctgccccagagcttcctgctcaagtgcttagagcaagtgaggaagatccagggcgatggc
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                                              Length 1521;
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interleukin-3; ss.
                                                                           Indels
Sequence 1521 BP; 304 A; 488 C; 402 G; 327 T; 0 other;
                                           Score 486.8; DB 7;
Pred. No. 2.7e-101;
0; Mismatches 7;
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                                            93.3%;
98.6%;
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237..238
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                                                           Best Local Similarity 98.6
Matches 491; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144
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0
                                                                                                                                                                                                                                              Human recombinant granulocyte colony-stimulating factor - causes differentiation of granulocytes and monocytes from bone
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1525;
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1525 BP; 303 A; 491 C; 402 G; 329 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                               Score 486.8; DB 9;
Pred. No. 2.7e-101;
0; Mismatches 7;
                                                                                                                                                                                         Warren MK;
/note="G in the CHU-2 clone"
[237
                               /*tag= e
/note="C in the CHU-2 clone"
                                                                                                                                                                                         Kawasaki ES,
                                                                                                                                                                                                                                                                                           Example; Fig 4; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                93.3%;
98.6%;
                                                                                                          87EP-0307114
                                                                                                                                 86US-0932037
86US-0895194
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                                                                                                                                                                                                                                                                      marrow progenitor cells
                                                                                                                                                                                      Devlin PE,
                                                                                                                                                                                                              WPI; 1988-051585/08.
P-PSDB; AAP81162.
                                                                                                                                                                   (CETU ) CETUS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                18-NOV-1986;
01-AUG-1986;
                                                                                                           11-AUG-1987;
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Best Local Simi
Matches 491;
                                                                                     24-FEB-1988
                                                              EP256843-A.
                                                                                                                                                                                      Devlin JJ,
                    conflict
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The cDNA insert of pP12 contains 11 more bases than the CHU-2 G-CSF clone. The major difference between this clone, derived from MIA PaCa-2, and CHU-2 clone is a 9 bp insertion in the CHU-2 clone between bases 237 and 238. There are two other differences: an A at position 588 (G in the CHU-2 clone) is a silent third base change, and a T at position 1237(C in the CHU-2 clone) in the 3' untranslated region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216
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                                                                                                                                                                                                                    contg. colony stimulating factor-1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.3%; Score 486.8; DB 10; 98.6%; Pred. No. 2.7e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O'Rourke E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                        Colony stimulating factor-1; pP12;
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P-PSDB; AAP95033.
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                                                                                                        AAN91086 standard;
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                                                                                                                                                                                                                    Plasmid pP12
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                       GCCCTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCTTTCCAGCGCCGGGCA
                CTGCAGGCCCTGGAAGGGATCTCCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTG
                                              GACGTCGCCGACTTTGCCACCACCATCTGGCAGCAGATGGAAGAACTGGGAATGGCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Poly:peptide with granulocyte colony stimulating factor activity obtd. by recombinant DNA procedures for treating haematopoietic
                                                                                                                                                                                                                                            Sequence of human granulocyte colony stimulating factor (hpG-CSF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The examples describe procedures for the designing of probhdF-CSF cDNA and genomic clones, both of which are claimed
                                                                                                                                                                                                                                                                    Haematopoietic disorders; therapy; aplastic anaemia;
bone marrow transplant; burn wounds; leukaemia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 22-24; 79pp; English.
                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                  Haematopoietic disorders; therapy;
                                                                                                                                                                                              BP.
                                                                                                                                                                                              AAN71089 standard; DNA; 1415
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85US-0768959.
85US-0768954.
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37..561
/*tag= .b
1797..1802
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23-AUG-1985;
23-AUG-1985;
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337
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                                                                                                                                                                                                              Gaps
Specifically claimed are DNA sequences encoding for (Ala 1)hpG-CSF; (Ser 36, 42, 64 and 74)hpG-CSF and the corresponding Met-1 cpds. The novelty is that hpG-CSF is the prod. of procaryotic or according encaryotic expression of an exagenous DNA sequence. The construction of hpG-CSF expression vectors is also described in the examples.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAGCTGTGCCACCCCGAGGAGCTGGTG
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                                                                                                                                                                        Length 1415;
                                                                                                                                                                                                                Indels
                                                                                                                 Sequence 1415 BP; 265 A; 451 C; 380 G; 319 T; 0 other;
                                                                                                                                                                        ; DB 8;
.2e-101;
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                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                        Score 485.2;
Pred. No. 6.2
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ne: 12566 sec
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BE558945 PII_84_EI BG556176 EMI_68_FO AA155622 co70d02.s ALI69742 Tetraodon AL106054 Drosophil

AA115932 2101210.s AA058743 2K70f07.s B1345642 374523 MA BB647049 BB647049 BF668325 292084 BA BW016196 603642649

B1345642 BB647049 BF868325 BM016196 BM474138 BG604563

BE463718 hx79f09.x AL178331 Tetracdon BE961002 MONOL_3_H BE960812 MONOL_1_B BE961242 MONOL_1_B AM193322 x173e08.x BE048584 hr50110.x AW175624 RC3_BE004

BE463718 CNS022LE BI961002

BI961242 AW193322

BE048584

BI960812

AW175624 AI818468 AW072844 AW273147

CNS0072Q BI410408 AW273202

A1818468 wk60c03.x AW072844 xa42g06.x AW273147 xr34c05.x

ALIGNMENTS

BM474138 AGENCOURT BG604563 WHE0947_C AL572931 AL572931 AL066742 Drosophil B1410408 602564928 AW273202 xr35c05.x

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numenal as Eutherias Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

S. NIH-MGC http://mgc.nci.nih.gov/.

S. NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Contact: Robert Strausberg, Ph.D.

Email: cgapba-remail.nih.gov

Tissue Procurement: DcTD/DTP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

http://image.llnl.gov

Right quality sequence stop: 542.

Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            990 bp mRNA linear EST 29-JAN-2002 5', mRNA sequence. BM423896.1 GI:18392108 EST. 29-JAN-2002 EM423896.1 GI:18392108 EST.
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/do_xref="taxon.9606"
/do_xref="taxon.9606"
/clone=lib="NIH_MGC_41"
/tissue_type="amelanotic melanoma, cell line"
/tab_nost="DH10B (phage-resistant)"
/note="Organ: Skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
into BeoxIX/AhoI sites using the following 5 adaptor:
GGCAGCAG(G): Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
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COMMENT
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KEYWORDS
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BE48194 172130 BA
BM009247 603629653
B1822673 6036396006
B1961002 MONOL_3_H
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BE480590 165716 BA
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                     GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NH_MGC Library." 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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                                                                                                                                              1;
                                                                                                            87.0%; Score 454.2; DB 10; Length 990; 95.6%; Pred. No. 9.7e-93; Live 0; Mismatches 21; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                 288 g
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//tissue_type="amelanotic melanoma, cell line"
//lab.host="DH10B (phage-resistant)"
//note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dr prining. Directionally cloudinto ECORI/XhoI sites using the following 5 adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 CTGCTCGGACACTCTCTGGGCATCCCCTGGGCTCCCCTGAGCAGCTGCCCCAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265 CTGCAGGCCCTGGAAGGGATCTCCCCCGAGTTGGGTCCCACCTTGGACAC-ACTGCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTACCACAGAGCTTCCTTTTAAAAAGCTTAGAGCAAGTGAGGAAGATCCAGGGCGATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 CTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATAGCGGCCTTTTCCTCTACCAGGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               660 GCCCTGCAAGCCCAACCCAATGTTGCCATGCCGGCTTCG-CTCTGCTTTCCAGCGCCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           444 AGGAGGGGTCCTAGTTGCCTCCCATCTGCAGAGCTTCCTGGAGGTGTCGTACCGCGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 384 TGCCCTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCTCTGCTTTCCAGCGCCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tch 74.3%; Score 387.8; DB 10; Length al Similarity 92.6%; Pred. No. 9.5e-78; 462; Conservative 0; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  150 t
                                                                      /organism-"Homo sapiens"
                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:5443757"
/clone_lib="NIH_MGC_41"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     570 bp
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MONO1_7_G12.b1_A005 Monocytes
sequence.
High quality sequence stop: 7 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           251 g
                                                                                                                                                                                                                                                                                                                                                                          NIH_MGC Library.
272 c 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       504 A-CGCCACCTTGCCCAGCC 521
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GI:16319015
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86.4%;
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                                                                                                                                        Equus caballus
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                                                                             BI960812
BI960812.1
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horse.
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ORIGIN
                                              DEFINITION
                                                                             ACCESSION
VERSION
                                                                                                                                      ORGANISM
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Isolated peripheral blood monocytes stimulated with E. coli lipopolysaccharide"
with E. coli lipopolysaccharide"
/note="Vector: pBluescript SK(-) from Lambda ZapII;
Site_1: Xhoi; Site_2: EcoRI; The library was made from poly.* RNA in the cloning vector lambda ZapII. Clones to be sequenced were prepared by mass excision."
202 c 167 g 101 t
                                                                                                                                The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Par. 706 542 1860
Fax. 706 542 1805
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
Sequences prime sequences, which are obtained with PolyTMIX or T7
sequencing primer, are presented as the reverse complement.
Seq primer: JEN REV
High quality sequence stop: 541
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                                               Wentzel, V.E.,
      Euteleostomi;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
1 (bases 1 to 570)
Vandenplas, M. L., Cordonnier-Pratt, M.-M., Sudman, M.L., V
Gingle, A.R., Pratt, L.H. and Moore, J.N.
An EST database from equine (Equus caballus) monocytes
Unpublished (2001)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 570;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 65.8%; Score 343.6; DB 1
Best Local Similarity 87.4%; Pred. No. 8.5e-68;
Matches 376; Conservative 0; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Monocytes (MONO1)"
                                                                                                                                                                                                                                                                                                                                             /organism="Equus caballus"
/db_xref="taxon:9796"
                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                        TITLE
JOURNAL
COMMENT
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                                              AUTHORS
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1. 548
/organism="Equus caballus"
/db.rafe="taxon:9796"
/clone_lib=="Monocytes (MONO1)"
/cell_type="Isolated peripheral blood monocytes stimulated
with E. coli lipopolysaccharide"
/note="Vector: pBluescript SK(-) from Lambda ZapII;
Site_1: XhoI; Site_2: EcoRI; The library was made from
poly-A RNA in the cloning vector lambda ZAPII. Clones to
be sequenced were prepared by mass excision."
  EST 22-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for high quality sequence is
20. Three-prime sequences, which are obtained with PolyTMix or T7
sequencing primer, are presented as the reverse complement.
Seq primer: JEN REV
High quality sequence stop: 481
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An EST database from equine (Equus caballus) monocytes
Unpublished (2001)
Contact: Cordonnier-Pratt MM
Department of Botany
Plan University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1860
Fax: 706 542 1860
                                                                                                                                                                                                      Vertebrata; Euteleostomi;
Jac Dp mkNa linear EST 22-OCT-: MONOL_1_B08.b1_A005 Monocytes (MONO1) Equus caballus cDNA, mRNA sequence.
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Pred. No. 2.8e-63;
0; Mismatches 56;
                                                                                                                                                                                                      Craniata;
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Perissodac
1 (bases 1 to 548)
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TITLE
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 197
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by:Incyte Genomics, Inc.

Clone distribution: NI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LlAM11287 row: o column: 18

High quality sequence start: 32

High quality sequence stop: 912.
                                                                                                                       B1411128 973 bp mRNA linear EST 14-AUG-2001
602962472F1 NCI_CGAP_Lu33 Mus musculus CDNA clone IMAGE:5118185 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaliai Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 973)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CONA. Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 AGCTGGTGTTGCTGGGCCACTCTCTGGGGATCCCGAAGGCTTCCCTGAGTGGCTGCTCTA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 GCGATGGCGCAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAGCTGTGCCACCCGAGG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 AGCTGGTGCTGCTCGGACACTCTCTGGGCATCCCCTGGGCTCCCCTGAGCAGCTGCCCCA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 CCTCGAGTCTACCACAGAGCTTCCTTTTAAAAAGCTTAGAGCAAGTGAGGAAGATCCAGG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5118185"
/tissue_type="pooled lung tumors"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .973
/organism="Mus musculus"
                                                                                                                                                                                        BI411128.1 GI:15172051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.4%;
ilarity 77.1%;
Conservative (
                                                                                                                                                        mRNA sequence.
                                                                                                                                                                                                                               house mouse
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Best Local S
                                                                                                                                      DEFINITION
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ORIGIN
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                          ACCESSION
                                                                                     RESULT
BI411128
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/organism="thomo sapiens"
/db_xref="texon:9606"
/clone="lib="NIH MGC_77"
/lab_host="bli0B (Tl phage-resistant)"
/note="Organ: lung, Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: lung, Vector: l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        598 bp mRNA linear EST 04-APR-2001 602575289F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4703159 5', BG548320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436
437 GCCGGGCAGGAGGGGTCCTAGTTGCCTCCCATCTGCAGAGCTTCCTGGAGGTGTCGTACC 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM1541 row: b column: 24
High quality sequence stop: 597.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                               317 TGCAGCTGGACGTCGCCGACTTTGCCACCACCATCTGGCAGCAGATGGAAGAACTGGGAA
                                                                                                                                                AGGGGCTCCTGCAGGCCCTGGAAGGGATCTCCCCCGAGTTGGGTCCCACCTTGGACACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       377 TGGCCCCTGCCCTGCAGCCCAGGGTGCCATGCCGGCCTTCGCCTCTGCTTTCCAGC
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          497 GCGTTCTACGCCACCTTGCCCAGCCC 522
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JOURNAL
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KEYWORDS
SOURCE
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BM009247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pcMV SPORT6; Site_1: Xbal; Site_2: Xhol;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 28-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                               267 GCAGGCCCTGGAAGGGATCTCCCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTGGA 326
                                                                                                                                                                                                  386
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                                                                                                                                                                                                                                                                                                 424
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Sonstegard,T.S., Capuco,A.V., Van Tassell,C.P., Ashwell,M.S.
                                                                 207 GCAGCTGGCAGGCTGCTTGAGCCAACTCCATAGCGGCCTTTTCCTCTACCAGGGGCTCCT
                                                                                                                                                  CGTCGCCGACTTTGCCACCACCATCTGGCAGCAGAAGAACTGGGAATGGCCCCTGC
                                                                                                                                                                                                                                                                  CCTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCTCTGCTTTCCAGCGCCGGGCAGG
                                                                                                                                                                                                                                                                                                 365 CCTGCAGCCCACCCAGGTGCCATGCCGGCCTTCGCCTCTGCTTTCCAGCGCCGGGCAGG
                                                                                                                                                                                                                                                                                                                                447 AGGGGTCCTAGTTGCCTCCCATCTGCAGAGCTTCCTGGAGGTGTCGTACGGCGTTCTACG
                                                                                                                                                                                                                                                                                   ö
   Length 598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3E485194 1inear 507 bp mRNA linear 172130 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
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                                    Indels
   DB 10;
Score 312.8; DB 1
Pred. No. 7.9e~61;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: 134 row: J column: 17
Seg primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: tads@lpsi.barc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="pooled"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gland cDNA library
Unpublished (2000)
Contact: Sonstegard TS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE485194.1 GI:9604727
 59.9%;
99.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                   CCACCTTGCCCAGCCC 500
                                                                                                                                                                                                                                                                                                                                                                                                507 CCACCTTGCCCAGCCC 522
                 Best_Local Similarity 99.4
Matches 314; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus
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   Query Match
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COMMENT
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KEYWORDS
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BM009247 829 bp mRNA linear EST 30-OCT-2001
603629663F1 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5434958 5',
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Righ quality sequence start: 7

High quality sequence start: 7

High quality sequence stop: 590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGTGCCACCTACAAGCTGTGCCACCCCGAGGAGCTGGTGCTGCTCGGACACTCTCTGGG 164
                                                                                                                                                                                                                                                                                          CATCCCCTGGGCTCCCCTGAGCAGCTGCCCCAGCCCAGGCCCTGCAGCTGGCAGGCTGCTT 224
                                                                                                                                                                                                                                                                                                                                                                                     GAGCCAACTCCATAGCGGCCTTTTCCTCTACCAGGGGCTCCTGCAGGCCCTGGAAGGGAT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               405 TGCCATGCCGGCCTTCGCCTTTCCAGCGCCGGGCAGGAGGGGTCCTAGTTGCCTC 464
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                   224 GAACCAACTACACGGCGCCCCTTTCTCTACCAGGGCCTCCTGCAGGCCCTGGCGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         344 GAACATCTGGCTGCAGATGGAGGACCTGGGGGCGCCCCCCGCTGTGCAGCCCCCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTGGACGTCGCCGACTTTGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345 CACCATCTGGCAGCAGATGGAAGAACTGGGAATGGCCCCTGCCCTGCAGCCCAGGG
                                                                                                                                          ;
                                                                                          Length 507;
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/clone_lib="NIH_MGC_41"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGCTGCATCGTTTCCTGGAGCTGGCATACCGTGGCCTGCGC 506
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                                                                                             DB 10;
                                                                                             Score 300.6; DB 1
Pred. No. 4.3e-58;
                                                                                                                                          0; Mismatches
82
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  158
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                                                                                             57.6%;
84.1%;
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                                                                                                                                               339; Conservative
170
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BM009247
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                                                                                                                      Similarity
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ECORI; CDNA made by oligo-dr priming. Directionally cloned thro EcoRIX/Xhol sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NH MG Library.
                                                                                                                                                                                                                   8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BI822673 94-OCT-2001 603036006F1 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5177209 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 948)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2
                                                                                                                                                                                                                                                                                                                                                                       200
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                                                                                                                                                                                                                   16;
                                                                                                                                                                                 Score 281.2; DB 10; Length 829;
Pred. No. 1.2e-53;
0; Mismatches 73; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                   53.9%;
82.5%;
                                                                                                                                                                                   Query Match 53.9
Best Local Similarity 82.5
Matches 421; Conservative
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Anotes Torgan: pooled brain, lung, testis; Vector:

PCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA

PCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA

PCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed);

male lung, age 27; and 1 male testis, age 69. Library is

oligo-dr primed and directionally cloned (EcoRV site is

destroyed upon cloning). Average insert size 1: 8 kb,

insert size range 1-3 kb. Library is normalized and

enriched for full-length clones and was constructed by C.

Gruber (Invitrogen). Research Genetics tracking code

021. Note: this is a NHL_MGC Library."
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM11441 row: k column: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.3%; Score 210.6; DB 10; Length 948; 70.1%; Pred. No. 1.1e-37; Live 0; Mismatches 39; Indels 150;
                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ImAGE:5177209"
/clone_lib="NHLMGC_115"
/lab_host="DH108"
                                                                                                 High quality sequence stop: 845.
Location/Qualifiers
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444; Conservative
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478 TICCTGGAGGTGTCGTACCGCGTTCTACGCCAC 510

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CDNA Library Preparation: Life Technologies, Inc.

EST 17-DEC-2001

10

RESULT

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BI961002

DEFINITION

ACCESSION VERSION

ORGANISM

REFERENCE AUTHORS

KEYWORDS SOURCE

TITLE JOURNAL COMMENT

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Single pass sequencing. Bases called and alt_trimmed with phred v0.980904. Wettor identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR PRIMERS
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="pooled"
/tlab_host="publish"
/hab_host="publish"
/note="vector: pcWv SPORT6; Site_1: Xba1; Site_2: Xho1;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendonosus muscle, and fetal
longissimus muscle."
1 181 c 147 g 86 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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         BM256261 509 bp mRNA linear 518592 MARC 3BOV BOS taurus CDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TT: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 150; DB 10;
Pred. No. 4.8e-24;
0; Mismatches 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 bp
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Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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                                                                                               BM256261.1 GI:17891860
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86.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l. 368
/organism="Equus caballus"
/organism="Equus caballus"
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/db.xref="Iib="Monocytes (MONOI)"
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/call_type="Isolated peripheral blood monocytes stimulated
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/rote="list"/>foot="vector: pBluescript SKr">foot="vector: pBluescript 
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Butheria; Perissodactyla; Equidae; Equus.

E (1) (Abases I to 368)
S Vandenplas,M.L., Cordonnier-Pratt,M.-M., Sudman,M.L., Wentzel,V.E., Gingle,A.R., Pratt,L.H. and Moore,J.N.
An EST database from equine (Equus caballus) monocytes
L Unpublished (2001)
Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1865
                                                                                                                                                                                  B1961002 368 bp mRNA linear EST 22-OCT-2001 MONOL_3_H01.bl_A005 Monocytes (MONO1) Equus caballus cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wentzel, V.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for high quality sequence is 20. Three-prime sequences, which are obtained with PolyTMix or T7 sequencing primer, are presented as the reverse complement. Seq primer: JEN REV High quality sequence stop: 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 181; DB 10; Length 368;
Pred. No. 4.4e-31;
0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 916 TTCCTGCAGGTGTACCCGGTATAGGGCAAC 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                              BI961002
BI961002.1 GI:16319205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.78;
86.98;
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Matches 199; Conserv
                                                                                                                                                                                                                                                 sequence.
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BASE COUNT

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EST 16-JAN-2001

RESULT 1 BM256261

DEFINITION ACCESSION

ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

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Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19016 of RPCI-98 library from Drosophila melanogaster (fruit AL053013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9796"
/clone_lib="Monocytes (MONO1)"
/clone_lib="Monocytes (MONO1)"
/cell_type="Isolated peripheral blood monocytes stimulated
/cell_type="Isolated" peripheral
/note="vector: pBluescript SK(-) from Lambda ZapII;
/note="vector: pBluescript SK(-) from Lambda ZapII;
/site_1: XhoI; Site_2: EcoRI; The library was made from
poly-A RNA in the cloning vector lambda ZAPII. Clones to
be sequenced were prepared by mass excision."

a 178 c 181 g 166 t lothers
                                                                                                                                                      1 (bases 1 to 673)
Vandenplas, M.L., Cordonnier-Pratt, M.-M., Sudman, M.L., Wentzel, V.E.,
Vandenplas, M.L., Cordonnier-Pratt, M.-M.,
An EST database from equine (Equus caballus) monocytes
Unpublished (2001)
Contact: Cordonnier-Pratt MM
Department of Botany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefêgenoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for high quality sequence is 50. Three-prime sequences, which are obtained with PolyTMix or T7 sequencing primer, are presented as the reverse complement. Seq primer: PolyTMix
                                                                         Equus caballus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  432 CCAGCGCCGGGCAGGAGGGGTCCTAGTTGCCTCCCATCTGCAGAGCTTCCTGGAGGTGTC 491
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1 (bases 1 to 925)
Genoscope.
                                                                                                                                                                                                                                                                                                                                           The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Exe: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 673;
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Pred. No. 2.2e-05;
0; Mismatches 15;
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High quality sequence stop: 673
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  GI:16320085
                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mmpratt@uga.edu
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83.5%;
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Les 76; Conservative
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Matches 76
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CNS0091P
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TITLE
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                                                                                                                                                              REFERENCE
                                                                                                                                                                                          AUTHORS
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// Organism="Homo sapiens"
// Ab_xref="taxon:9606"
// Clone_lib="Eaxon:9606"
// Act_stage="Adult"
// Act_organ: lung_normal; Vector: puc18; Site_l: SmaI;
// Act_organ: lung_normal; Vector: puc18; Site_l: SmaI;
// Site_l: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
103 g 76 t
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MONOL_7_G12.g1_A005 Monocytes (MONO1) Equus caballus CDNA, mRNA
sequence.
                                                                                                                                                                                                          1 (bases 1 to 327)
Jaks Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: asimpsofoldwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This unity can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=0V0&t2=QV0-EN0102-081100-458-906&t3=2000-11-08&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 327.
  QVO-EN0102-081100-458-906 EN0102 Homo sapiens CDNA, mRNA sequence.
                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 327)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 GCTCCTGCAGGCCCTGGAAGGGATCTCCCCCGAGTTGGGTCCCCACCTTGGACACACTGCA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 GGCCCTGCAGCTGCAGGCTGCTTGAGCCAACTCCATAGCGGCCTTTTCCTCTACCAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 7e-21;
); Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                        BF848766.1 GI:12235903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.0%;
89.6%;
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Matches 146;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library fillers for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
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/db_xxef="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACRI9D16"
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Wells K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library
Unpublished (2000)
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bd19: 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Exx: 301 504 8414
Email: tads@lpsi.barc.usda.gov
                                                                                                                                                                                                                                                                                                                                                    Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pCMV SPORT6; Site_1: Xbal; Site_2: Xhol;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                  [ (bases 1 to 513)
Sonstegard,T.S., Capuco,A.V., Van Tassell,C.P., Ashwell,M.S.
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Pred. No. 0.18;
0; Mismatches 13;
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/clone_lib="BARC 5BOV"
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BACKWARD: GTTTCCCAGTCACGACG
Plate: 17 row: C column: 20
Seq primer: ATTTAGGTGACACTATAG
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/lab_host="DH10B"
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1 Similarity 81.7%;
58; Conservative
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|GCCGAGCTGCA 513
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                          AUTHORS
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                            C12N15/58, C12N15/70, C12N15/85, C12P21/02, C12P21/02, (C12N1/21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product='human colony-stimulating factor
                                                                                                                                                                                                                                                                                                                GTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAAGCTGTGTGCCCACCTACAAG 120
                                                                                                                                                                                                                                                                                                                         61 GTGAGGAAGATCCAGGGGGATGGCGCAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 GCCCTTTTCCTCTACCAGGGCTCCTGCAGGCCCTGGAAGGGATCTCCCCCGAGTTGGGT 300
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                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                   241 GGCCTTTTCCTCTACCAGGGCTCCTGCAGGCCCTGGAAGGGATCTCCCCCCGAGTTGGGT
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DNA encoding human colony-stimulating factor derivative.
E02575
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                                                                                                                                                                                                                                      Length 525;
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                                            (C12P21/02,C12R1:19),(C12P21/02,C12R1:91);
                                                                                                                                                'hG-CSF[ND28]''
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGAGGTGTCGTACCGCGTTCTACGCCCACTTGCCCAGCCC 522
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9
                                                                                                                                              Location/Qualifiers
1. 525
/organism="synthetic construct"
/db_xref="taxon:32630"
a 184 c 148 g 99 t
                                                                                                                                                                                                                                   99.7%; Score 520.4; DB 6; illarity 99.8%; Pred. No. 8.8e-87; Conservative 0; Mismatches 1;
                                                                                                Location/Qualifiers
                                                                                                                                       derivative which
                                                        strandedness: Double;
topology: Linear;
hypothetical: No;
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JP 1990227075-A/3.
synthetic construct.
                                                                                       anti-sense: No;
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  Query Match
Best Local Simi
Matches (521;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product='human colony-stimulating factor derivative(hG-CSF[ND28N6]) which is resistant to proteases'.
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                                                                                                                                                                                                      29-SEP-1988 JP 88P 245705
SASAKI KATSUTOSHI, NISHI TATSUYA, YASUMURA SHIGEYOSHI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                ITOU SEIGA
C12N9/72, C07K13/00, C07K15/14, C12N1/21, C12N5/10, C12N9/64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GCGCCAACATATCGCGCCTCGAGTCTACCACAGAGCTTCCTTTTAAAAAGCTTAGAGCAA
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0
synthetic construct
artificial sequence.
1 (bases 1 to 525)
Sasaki,K., Mshi,T., Yasumura,S., Sato,M. and Itou,S.
NEW POLYPEPTIDE
Patent: JP 1990227075-A 3 10-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.5%; Score 514; DB 6; Length 525; 99.0%; Pred. No. 1.3e-85; Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                     C12R1:19),
(C12P21/02,C12R1:19),(C12P21/02,C12R1:91);
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/organism="synthetic construct"
/db_xref="taxon:32630"
183 c 148 g 100 t
                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                   XYOWA HAKKO KGGYO CO LTD
OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1990227075-A/3
PD 10-SEP-1990
PF 28-SEP-1989 JP 1989253097
PR 29-SEP-1988 JP 88P 245705
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topology: Linear;
hypothetical: No;
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Best Local Similarity 99.0
Matches 517; Conservative
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181 CTGAGCAGCTGCCCCAGCCCAGGCCCTGCAGCTGCTGCTTGAGCCAACTCCATAGC 240
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                                                                                                  ATGGAAGAACTGGGAATGGCCCCTGCCGCCCACCCAGGGTGCCATGCCGGCCTTC
                                            301 CCCACCTTGGACACACACTGCAGCTGGACGTCGCCGACTTTGCCACCACCATCTGGCAGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kuga,T., Miyaji,H., Sato,M., Okabe,M., Morimoto,M., Yamasaki,M., Yokoo,Y., Yamaguchi,K., Yoshida,H. and Polypeptide derivatives of human granulocyte colony factor
                                                                                                                                                                                                                                                                 Score 486.8; DB 6;
Pred. No. 1.4e-80;
0; Mismatches 7;
                                                                                                                                                                                                                                                    CTGGAGGTGTCGTACGCGTTCTACGCCACCTTGCCCAGCCC
                                                                                                                                                                                                                                                                                                                                                              Sequence 1 from patent US 5795968.
AR024358
AR024358.1 GI:3977652
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1. .525
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192 c 151 g
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98.6%;
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Matches 491; Conserv
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/product='human colony-stimulating factor
GCCTCTGCTTTCCAGCGCCGGGCAGGGGGTCCTAGTTGCCTCCCATCTGCAGAGCTTC 480
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                                                                                                                                                                                                                                                                                                                                                                                                                               C12N9/72, C07K13/00, C07K15/14, C12N1/21, C12N5/10, C12N9/64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (hG-CSF[ND28N145]) which is resistant to
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                                                                                                                                                                                                                                                                                                                                                           28-SEP-1889 JP 1989253097
29-SEP-1988 JP 88P 245705
SASAKI KATSUTOSHI, NISHI TATSUYA, YASUMURA SHIGEYOSHI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                      artificial sequence.
1 (bases 1 to 525)
Sasaki,K., Nishi,T., Yasumura,S., Sato,M. and Itou,S.
NEW POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 525;
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                        Score 512.4; DB 6;
Pred. No. 2.6e-85;
); Mismatches 6;
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/organism="synthetic construct"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                            Patent: JP 1990227075-A 4 10-SEP-1990;
KYOWA HAKKO KOGYO CO LTD
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                                                                                                                                                                                                                                                                                                        Artificial gene
Artificial sequence; Genes.
JP 1990227075-A/4
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182 c 146 g
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Best Local Similarity 98.9%;
Matches 516; Conservative (
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JP 1990227075-A/4.
                                                                                                                                                                                          synthetic construct.
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ACCESSION
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ORIGIN
                                                                                                                                                                                                                                                            TITLE
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PAT 05-DEC-1998

Itoh, S., | Komatsu, Y.

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Gaps 84

Length Indels 204

264 324

PAT 29-SEP-1997

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JP 1988267292-A/1
04-NOV-1988
23-DEC-1987 JP 1987326384
23-DEC-1986 JP 86P 306799
KUGA TETSUO, KOMATSU YUKI, MIYAJI HIROMASA, SATO MORIYUKI, PI
                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                        MORINOTO MAKOTO, ITOU SEIGA, YAMAZAKI MOTOO, YOKOO YOSHIHARU
YAMAGUCHI KAZUO
C12P21/02,C07K13/00,C12N1/20,C12N15/00//A61K37/02,A61K37/02,
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostor
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 525)
Kuga, T., Komatsu, Y., Miyaji, H., Sato, M., Okabe, M., Morimoto, M.
Itou, S., Yamazaki, M., Yokoo, Y. and Yamaguchi, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 GCAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAGCTGTGCCACCCCGAGGAGCTGGTG 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product='mature peptide of hG-CSF'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 525;
                                                                                                  cDNA encoding hG-CSF form human periferal macrophage.
E01731
E01731. I GI:2169984
JP 1988267292-A/1.
                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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strandedness: Double;
topology: Linear;
hypothetical: No;
*source: cell_line-Periferal macrophage;
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Pred. No. 1.4e-80;
0; Mismatches 7;
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                                                                                                                                                                                                                                                      Patent: JP 1988267292-A 1 04-NOV-1988;
KYOWA HAKKO KOGYO CO LTD
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 192 c 151 g 9:
                                                                                        525 bp
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98.6%;
CGCCACCTTGCCCAGCCC 522
             505 CGCCACCTTGCCCAGCCC 522
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Homo sapiens
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Patent: US 5994518-A 1 30-Nov-1999;
Location/Qualifiers
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Pred. No. 1.4e-80;
0; Mismatches 7; Indels 0
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                                                                                                                                                                                                   Sequence 1 from patent US 5994518.
AR091731.1 GI:10018485
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192 c 151 g
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98.6%;
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Gaps

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84 84 204

204 264

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S Kuga, T., Komatsu, Y., Miyaji, H., Sato, M., Okabe, M., Morimoto, M., Itou, S., Yamazaki, M., Yokoo, Y. and Yamaguchi, K. .

NGW POLYPEPTIDE
L. Patent: JP 1994092994-A 1 05-APR-1994;

KYOWA HAKKO KOGYO CO LTD
OS HOMO Saplens (human)
PN JP 1994092994-A/1
PD 05-APR-1994
PF 23-DEC-1987 JP 1992214376
PR 23-DEC-1986 JP 86P 306799
PI KUGA TETSUO, KOMATSU YUKI, MIYAJI HIROMASA, SATO MORIYUKI, PI OKABE MASAMI.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 525)
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    GCAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAGCTGTGCCACCCCGAGGAGCTGGTG
                                                                                                   GCCCTGCAGCCCAGGGTGCCATGCCGGCCTTCGCCTCTGCTTTCCAGCGCCGGGCA
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                                                                                                                                                                                                                                                                                                                                           linear
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/cell_type='macrophage'
/clone='pCSF1-2'
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topology: Linear;
hypothetical: No;
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JP 1994092994-A/1.
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Homo sapiens
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C12N15/58,C12N15/70,C12N15/85,C12P21/02,C12P21/02,(C12N1/21,
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                      F
GACGTCGCCGACTTTGCCACCACCATCTGGCAGCAGATGGAAGAACTGGGAATGGCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hon
1 (bases 1 to $25)
Sasaki,K., Nishi,T., Yasumura,S., Sato,M. and Itou,S.
NEW POLYPEPTIDE

    .522 | human colony-stimulating

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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(C12P21/02,C12R1:19), (C12P21/02,C12R1:91);
strandedness: Double;
topology: Linear;
hypothetical: No;
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*source: clone=pCSF1-2;
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Pred. No. 1.4e-80;
); Mismatches 7;
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Location/Qualifiers
1. 525
/organism="Homo sapiens"
/db_xref="taxon:9606"
a 192 c 151 g 97
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llarity 98.6%;
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JP 1990227075-A/1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 525)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kuga_T., Komatsu,Y., Miyaji,H., Sato,M., Okabe,M., Morimoto,M.,
Itou,S., Yamazaki,M., Yokoo,Y. and Yamaguchi,K.
NEW POLYPEPTIDE
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Human mRNA for granulocyte-colony stimulating factor.
E15131
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1. .525
/product='human G-CSF'
Location/Qualifiers
                                                                                                      Score 486.8; DB 6;
Pred. No. 1.4e-80;
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/organism="Homo saplens"
/db_xref="taxon:9606"
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JP 1998052281-A/1.
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11 KUGA TETSUO, KOMATSU YUKI, MIYAJI HIROMASA, SATO MORIYUKI, PI
OKABE MASAMI,
                                        MORIMOTO MAKOTO, ITOU SEIGA, YAMAZAKI MOTOO, YOKOO YOSHIHARU,
YAMAGUCHI KAZUO
C12N15/09,A61K38/00,C07K14/535,C12N1/21,C12P21/02,(C12P21/02,
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/cell_type='peripheral blood macropharge'
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Location/Qualifiers
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Sequence 1 from patent US 5681720.
171150
171150.1 GI:3007285
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/organism="Homo sapiens"
/db_xref="taxon:9606"
| 192 c 151 g 97
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strandedness: Double;
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/organism="unknown"
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Kuga,Tr., Miyaji,H., Sato,M., Okabe,M., Morimoto,M., Itoh,S.,
Yamasaki,M., Yokoo,Y., Yamaguchi,K., Yoshida,H. and Komatsu,Y.
DNA encoding human granulocyte colony stimulating factor plasmids
and host cells comprising same, and methods of expressing the
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Komatsu, Y.
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Kuga.r., Miyaji,H., Sato,M., Okabe,M., Morimoto,M.,
Yamasaki,M., Yokoo,Y., Yamaguchi,K., Yoshida,H. and
Polypeptide derivatives of human granulocyte colony
factor
Patent: US 5714581-A 1 03-FEB-1998;
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Pred. No. 1.4e-80;
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Patent: US 5681720-A 1 28-OCT-1997;
Location/Qualifiers
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Sequence 1 from patent US 5714581.
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192 c 151 g
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ilarity 98.6%;
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Unclassified
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                                                                   Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 Length 525
                            Indels
Score 486.8; DB 6;
Pred. No. 1.4e-80;
0; Mismatches 7;
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Last updated, Version
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KYOWA HAKKO KOGYO CO LTD.
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1-525
1-626
1. Komatsu Y., Miyaji H., Sato P.
Yamazaki M., Yokoo Y., Yamaguchi K.;
"NEW POLYPEPTIDE";
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93.3%;
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                            491; Conservative
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granulocyte colony stimulating factor mRNA,
                                                                                                                                 J. Leukoc. Biol. 41, 302-306 (1987)
87196936
                                                                                                                                                              1. .660
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="G1:183041"
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           M17706
M17706.1 GI:183040
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                                                al.), clone pP12.
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                                                                       MORIMOTO MAKOTO, ITOU SEIGA, YAMAZAKI MOTOO, YOKOO YOSHIHARU,
                                                                                          C07K14/535,C12N1/21,C12N15/09,C12P21/02//A61K38/00,(C12N1/21,
                                                                                                                                                                                                                                                                                                                        25 CTACCACAGAGCTTCCTTTTAAAAGCTTAGAGCAAGTGAGGAAGATCCAGGGCGATGGC
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23-DEC-1986 JP 86P 306799
KUGA TETSUO, KOMATSU YUKI, MIYAJI HIROMASA, SATO MORIYUKI,
OKABE MASAMI,
                                                                                                                                                                                                                                                                        Score 486.8; DB 23; Length 525;
Pred. No. 1.4e-80;
0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                               Sequence 525 BP; 85 A; 192 C; 151 G; 97 T; 0 other;
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98.6%;
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       to sapiens (Human)
1995149798-A/1
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Matches 491; Conservative
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                                                                                                                                topology: Linear;
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                          13-JUN-1995
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Gclsolhsglflyggllgalegispelgptldtlolddafattimoomeelgmapal
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                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (asses 1 to 660)
Devlin, J. J., Devlin, P. E., Myambo, K., Lilly, M. B., Rado, T. A. and
                                                                                                                                                                                                                                             Expression of granulocyte colony-stimulating factor by human cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43. .657
/note="granulocyte colony stimulating factor precursor"
/codon_start=1
                               of Kawasaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="granulocyte colony stimulating factor signal
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243 c 188 q 113 t
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granulocyte colony stimulating factor.
Human MIA PaCa-2 cell line, cDNA to mRNA, (library
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PAT 29-SEP-1997
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1 (bases 1 to 1521)
Yamazaki,T., Yamamoto,O., Hirata,Y., Sekimori,Y. and Osada,J. .
POVET POLYPEPTIDE
Patent: JP 1987129298-A 11-JUN-1987;
CHUGAI PHARMACEUT CO LTD
                                                                                                                                                           385 CTGCAGGCCCTGGAAGGGATCTCCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTG 444
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                          GGAGGGGTCCTAGTTGCCTCCCATCTGCAGAGCTTCCTGGAGGTGTCGTACCGCGTTCTA
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/note='human G-CSF prewsor'
121. .642
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C07K13/00,C07H21/04,C12N15/00,C12P21/02;
strandedness: Double;
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/product='human G-CSF'
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Pred. No. 1.2e-80;
0; Mismatches 77;
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/note='human G-CSF'
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/organism="Homo sapiens"
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489 c 401 g 327
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02-DEC-1985 JP 1985269455
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hypothetical: No;
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JP 1987129298-A/1.
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Best Local Similarity 98.6
Matches 491; Conservative
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                                                                                                              HSGCSFR1 1498 bp mRNA linear PRI 21-MAR-1995 Human mRNA for granulocyte colony-stimulating factor (G-CSF) (PBRV-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/product="G-CSF protein"
/product="G-CSF protein"
/protein_id="Ca27290.1"
/db_xref="G1:732764"
/db_xref="SWISS-PROT:P09919"
/tcnslation="MAGPATOSPMKLMALQLLLWHSALWTVOBATPLGPASSLPQSFL
IKCLEVPK IGGDGALLQERLCATYKLCHPEELVLGHSLGIPWAPLSSCPSQALQLA
GCLSQLHSGLETYGGLLQALEGTSPELGPTLDTLQLVYADFATTIWQOMEELGMAPAL
OPTOGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP"
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                                                                                                                                                                                                                                                                      Nagata, S., Tsuchiya, M., Asano, S., Yamamoto, O., Hirata, Y., Kubota, N., Oheda, M., Nomura, H. and Yamazaki, T. The chromosomal gene structure and two mRNAs for human granulocyte
                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1498)
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/product="mature G-CSF protein (aa 1-174)"
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Pred. No. 1.2e-80;
0; Mismatches 7;
                                                                                                                                                                                     factor; signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="polyadenylation signal" 1498
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488 c 402 g 327 t
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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EMBO J. 5 (3), 575-581 (1986)
86220137
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